

WHAT IS CLAIMED IS:

1. An isolated or purified nucleic acid comprising a nucleotide sequence having at least 70% homology as measured by BLASTN version 2.0 set at the default parameters with a nucleotide sequence selected from the group consisting of SEQ ID NOS:18-34 and the nucleotide sequences complementary to SEQ ID NOS:18-34 or fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, 500, 750, 1000, 1250, or 1500 consecutive nucleotides thereof.
2. The nucleic acid according to claim 1, wherein the nucleic acid has at least 80% homology.
3. The nucleic acid according to claim 1, wherein the nucleic acid has at least 85% homology.
4. The nucleic acid according to claim 1, wherein the nucleic acid has at least 90% homology.
5. The nucleic acid according to claim 1, wherein the nucleic acid has at least 95% homology.
6. The nucleic acid according to claim 1, wherein the nucleic acid has at least 97% homology.
7. The nucleic acid according to claim 1, wherein the nucleic acid has 100% homology.
8. An isolated or purified nucleic acid comprising a nucleotide sequence having at least 70% homology as measured by BLASTN version 2.0 set at the default parameters with a nucleotide sequence selected from the group consisting of SEQ ID NOS:35-51 and the nucleotide sequences complementary to SEQ ID NOS:35-51, or fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, 500, 750, 1000, 1250, or 1500 consecutive nucleotides thereof.
9. The nucleic acid according to claim 8, wherein the nucleic acid has at least 80% homology.
10. The nucleic acid according to claim 8, wherein the nucleic acid has at least 85% homology.
11. The nucleic acid according to claim 8, wherein the nucleic acid has at least 90% homology.
12. The nucleic acid according to claim 8, wherein the nucleic acid has at least 95% homology.
13. The nucleic acid according to claim 8, wherein the nucleic acid has at least 97% homology.

14. The nucleic acid according to claim 8, wherein the nucleic acid has 100% homology.
15. An isolated or purified nucleic acid encoding a polypeptide having at least 25% amino acid identity as measured by BLASTP, BLASTX, or TBLASTN with default parameters with an amino acid sequence selected from the group consisting of SEQ ID NOS:52-68, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 200, 400, 600, 800, or 1000 consecutive amino acids thereof.
16. The nucleic acid according to claim 15, wherein the polypeptide has at least 40% homology.
17. The nucleic acid according to claim 15, wherein the polypeptide has at least 50% homology.
18. The nucleic acid according to claim 15, wherein the polypeptide has at least 60% homology.
19. The nucleic acid according to claim 15, wherein the polypeptide has at least 70% homology.
20. The nucleic acid according to claim 15, wherein the polypeptide has at least 80% homology.
21. The nucleic acid according to claim 15, wherein the polypeptide has at least 85% homology.
22. The nucleic acid according to claim 15, wherein the polypeptide has at least 90% homology.
23. The nucleic acid according to claim 15, wherein the polypeptide has at least 95% homology.
24. The nucleic acid according to claim 15, wherein the polypeptide has at least 99% homology.
25. The nucleic acid according to claim 15, wherein the polypeptide has 100% homology.
26. An isolated or purified polypeptide having at least 25% amino acid identity as measured by BLASTP, BLASTX, or TBLASTN set at default parameters with an amino acid sequence selected from the group consisting of SEQ ID NOS:52-68, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 200, 400, 600, 800, or 1000 consecutive amino acids thereof.
27. The polypeptide according to claim 26, wherein the polypeptide has at least 40% homology.

28. The polypeptide according to claim 26, wherein the polypeptide has at least 50% homology.
29. The polypeptide according to claim 26, wherein the polypeptide has at least 60% homology.
30. The polypeptide according to claim 26, wherein the polypeptide has at least 70% homology.
31. The polypeptide according to claim 26, wherein the polypeptide has at least 80% homology.
32. The polypeptide according to claim 26, wherein the polypeptide has at least 90% homology.
33. The polypeptide according to claim 26, wherein the polypeptide has at least 95% homology.
34. The polypeptide according to claim 26, wherein the polypeptide has at least 99% homology.
35. The polypeptide according to claim 26, wherein the polypeptide has 100% homology.
36. A recombinant nucleic acid comprising a nucleotide sequence encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS:52-68 operably linked to a promoter.
37. A genetically modified rice plant wherein a gene selected from the group consisting of germin-like protein, alternative oxidase (AOX1a) protein, XA21-like protein kinase gene, receptor-like protein kinase, methylmalonate semi-aldehyde dehydrogenase (MMSDH1), homolog of the RNA-binding protein LAH1, vacuolar ATP synthase subunit C, cinnamic acid 4-hydroxylase, H-protein promoter binding factor-2a, flap endonuclease (FEN-1), heat shock protein Hsp70, ammonium transporter, ATP-dependent RNA helicase, glucose-6-phosphate/phosphate transporter, RNA methyltransferase, actin depolymerizing factor 5, and beta-glucosidase has been disrupted.
38. A genetically modified rice plant wherein a gene comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:18-34 has been disrupted.
39. A genetically modified rice plant wherein a gene encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS:52-68: has been disrupted.

40. A genetically modified rice plant selected from the group consisting of 1b-115-22, 1b-164-43, 1b-192-40, 1b-207-27, 1b-138-07, 1d-059-12, 1c-087-40, 1c-017-14, 1c-038-56, 1c-041-47, 1c-064-20, 1c-109-35, 1c-109-51, 1c-056-07, 1c-100-32, 1c-142-27, and 1c-140-04.

41. A genetically modified rice plant which overexpresses or underexpresses a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS:52-68.

42. A method of screening a rice plant for a desirable characteristic comprising:

- a) obtaining a rice plant wherein a gene selected from the group consisting of SEQ ID NOS:18-34 has been disrupted; and
- b) exposing said rice plant to conditions which permit plants possessing said desirable characteristic to be identified.

43. The method of Claim 42, wherein said desirable characteristic to be identified is selected from the group consisting of: altered photosynthetic capacity, altered response to biotic stress, allelopathy, altered response to abiotic stress, altered morphology, altered grain yield, altered nutritional content of grain, altered growth rates, altered secondary product pathways, altered pesticide resistance, altered grain characteristics such as grain shape or taste, cooking quality, altered harvesting qualities, altered optimal growth temperatures, altered resistance to herbicides, altered flowering time, altered seed fill characteristics, altered hormone biosynthetic/degradation pathways, or altered responses to hormones.

44. A method of producing a genetically modified plant having an altered phenotype as compared to a wild-type plant, comprising:

- a) contacting a plant cell with a nucleic acid sequence which increases or decreases the expression or activity of a protein comprising an amino acid sequence selected from the group consisting of SEQ ID NOS:52-68 relative to a wild type plant to obtain a transformed plant cell;
- b) producing a plant from said transformed plant cell; and
- c) selecting a plant expressing said protein.

45. The method of Claim 44, wherein the contacting is by physical means.

46. The method of Claim 44, wherein the contacting is by chemical means.

47. The method of Claim 44, wherein the plant cell is selected from the group consisting of protoplasts, gamete producing cells, and cells which regenerate into whole plants.

48. The method of Claim 44, wherein the nucleic acid sequence is operably linked to a promoter selected from the group consisting of a constitutive promoter, a tissue specific promoter, an organ specific promoter, a developmentally specific promoter, and an inducible promoter.

49. The method of claim 44, wherein the promoter is selected from the group consisting of an endogenous promoter and a heterologous promoter.

50. The genetically modified plant of Claim 44, wherein the amino acid comprises at least 90% amino acid identity as measured by BLASTP, BLASTX, or TBLASTN with default parameters to a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS:52-68.

51. The genetically modified plant of Claim 44, wherein the amino acid comprises at least 95% amino acid identity as measured by BLASTP, BLASTX, or TBLASTN with default parameters to a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS:52-68.

52. The genetically modified plant of Claim 44, wherein said nucleic acid sequence encoding the protein comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:18-34 and SEQ ID NOS:35-51.

53. The genetically modified plant of Claim 44, wherein the plant is a dicotyledonous plant.

54. The genetically modified plant of Claim 44, wherein the plant is a monocotyledonous plant.

55. A genetically modified seed, into which a nucleic acid sequence encoding a polypeptide having at least 80% amino acid identity as measured by BLASTP, BLASTX, or TBLASTN set at default parameters to an amino acid sequence selected from the group consisting of SEQ ID NOS:52-68 has been introduced.

56. The genetically modified seed of Claim 55, wherein the nucleic acid encodes a polypeptide having at least 85% amino acid identity as measured by BLASTP, BLASTX, or TBLASTN set at default parameters to an amino acid amino acid sequence selected from the group consisting of SEQ ID NOS:52-68.

57. The genetically modified seed of Claim 55, wherein the nucleic acid encodes a polypeptide having at least 90% amino acid identity as measured by BLASTP, BLASTX, or TBLASTN set at default parameters to an amino acid amino acid sequence selected from the group consisting of SEQ ID NOS:52-68.

58. The genetically modified seed of Claim 55, wherein the nucleic acid encodes a polypeptide having at least 95% amino acid identity as measured by BLASTP, BLASTX, or TBLASTN set at default parameters to an amino acid amino acid sequence selected from the group consisting of SEQ ID NOS:52-68.

59. An antibody which binds to an isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS:52-68 or fragments thereof.

60. A method of expressing a gene in a desired tissue or organ of a rice plant comprising:

a) obtaining the promoter which directs the transcription of a sequence selected from the group consisting of SEQ ID NOS:18-34;

b) operably linking said promoter to said gene; and

c) introducing said promoter operably linked to said gene into a rice plant.

61. A computer readable medium comprising a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:18-34, the nucleotide sequences complementary to SEQ ID NOS:18-34, or fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, 500, 750, 1000, 1250, or 1500 consecutive nucleotides thereof stored thereon.

62. A computer readable medium of Claim 61, wherein the computer readable medium further comprises data indicating the tissue or organ in which the nucleic acid sequences are transcribed.

63. A computer readable medium comprising a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:35-51, the nucleotide sequences complementary to SEQ ID NOS:35-51, or fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, 500, 750, 1000, 1250, or 1500 consecutive nucleotides thereof stored thereon.

64. A computer readable medium of Claim 63, wherein the computer readable medium further comprises data indicating the tissue or organ in which mRNA having the coding sequence is expressed.

65. A computer readable medium comprising an amino acid sequence comprising an amino acid sequence selected from the group consisting of SEQ ID NOS:52-68, the nucleotide sequences complementary to SEQ ID NOS:52-68, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 200, 400, 600, 800, or 1000 consecutive amino acids thereof stored thereon.

66. A computer readable medium of Claim 65, wherein the computer readable medium further comprises data indicating the tissue or organ in which the amino acid sequence is present.